

Amendments to the Specification:

Please replace paragraph [0057] with the following amended paragraph:

[0057] Another example of a method of codon optimization is based on the direct use, without performing any extra statistical calculations, of codon optimization tables such as those provided on-line at the Codon Usage Database through the NIAS (National Institute of Agrobiological Sciences) DNA bank in Japan (<http://www.kazusa.or.jp/codon/>). The Codon Usage Database contains codon usage tables for a number of different species, with each codon usage table having been statistically determined based on the data present in Genbank. For example, the following table (located at [http://www.kazusa.or.jp/codon/cgi-bin/showcodon.cgi?species=Oryza+sativa+\(japonica+cultivar-group\)+\(gbpln\)](http://www.kazusa.or.jp/codon/cgi-bin/showcodon.cgi?species=Oryza+sativa+(japonica+cultivar-group)+(gbpln))) may be used for codon optimization of transgenes that are to be expressed in japonica cultivar rice plants:

Oryza sativa (japonica cultivar-group) [gbpln]: 32630 CDS's (12783238 codons)

fields: [triplet] [frequency: per thousand] ([number])

UUU 13.6(173985)	UCU 12.5(159540)	UAU 10.3(131821)	UGU 6.5(82520)
UUC 21.9(279329)	UCC 15.6(199591)	UAC 14.7(188349)	UGC 12.1(154274)
UUA 6.4(82284)	UCA 11.8(150624)	UAA 0.6(8057)	UGA 1.1(14199)
UUG 15.0(192153)	UCG 12.0(153755)	UAG 0.8(10388)	UGG 14.3(183072)
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CUU 14.9(190177)	CCU 13.8(175845)	CAU 11.6(148589)	CGU 8.0(101835)
CUC 24.2(309923)	CCC 12.3(156817)	CAC 13.9(178202)	CGC 16.3(208778)
CUA 8.0(102568)	CCA 14.4(184035)	CAA 14.3(183412)	CGA 7.6(96761)
CUG 20.1(256688)	CCG 17.7(226399)	CAG 20.6(263543)	CGG 14.1(180051)
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AUU 14.5(184754)	ACU 11.0(140200)	AAU 15.1(192829)	AGU 8.8(112594)
AUC 19.2(245629)	ACC 15.0(191716)	AAC 18.2(233034)	AGC 15.4(197340)
AUA 8.9(113169)	ACA 11.7(148967)	AAA 16.7(213264)	AGA 10.9(138985)
AUG 23.4(298881)	ACG 11.6(148202)	AAG 31.9(408318)	AGG 15.8(202111)
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GUU 15.5(197654)	GCU 19.6(250883)	GAU 25.5(326196)	GGU 14.9(189844)
GUC 19.7(251434)	GCC 30.1(385150)	GAC 27.9(356336)	GGC 28.5(364371)
GUA 7.1(90381)	GCA 17.6(224608)	GAA 22.6(289123)	GGA 16.4(210234)
GUG 23.8(304169)	GCG 26.0(332493)	GAG 38.6(493349)	GGG 17.2(219456)

Coding GC 55.04% 1st letter GC 58.27% 2nd letter GC 46.04% 3rd letter GC 60.81%

Please replace paragraph [0061] with the following amended paragraph:

[0061] The present invention encompasses sequences that are similar or substantially identical to a coding sequence or modified coding sequence of GM-CSF. By "substantially identical" is meant any nucleotide sequence with similarity to the genetic sequence of GM-CSF, or a fragment or a derivative thereof. The term "substantially identical" can also be used to describe similarity of polypeptide sequences. For example, nucleotide sequences or polypeptide sequences that are greater than about 70%, preferably greater than about 80%, more preferably greater than about 70% identical to the GM-CSF coding sequence or the encoded

polypeptide, respectively, and still retain GM-CSF activity are contemplated. To determine whether a nucleic acid exhibits similarity with the sequences presented herein, oligonucleotide alignment algorithms may be used, for example, but not limited to a BLAST (GenBank URL: www.ncbi.nlm.nih.gov/cgi-bin/BLAST/, using default parameters: Program: blastn; Database: nr; Expect 10; filter: default; Alignment: pairwise; Query genetic Codes: Standard(1)), BLAST2 (EMBL URL: <http://www.embl-heidelberg.de/Services/index.html> using default parameters: Matrix BLOSUM62; Filter: default, echofilter: on, Expect:10, cutoff: default; Strand: both; Descriptions: 50, Alignments: 50), or FASTA, search, using default parameters. Polypeptide alignment algorithms are also available, for example, without limitation, BLAST 2 Sequences (www.ncbi.nlm.nih.gov/blast/bl2seq/bl2.html, using default parameters Program: blastp; Matrix: BLOSUM62; Open gap (11) and extension gap (1) penalties; gap x_dropoff: 50; Expect 10; Word size: 3; filter: default).